

Fig. 1

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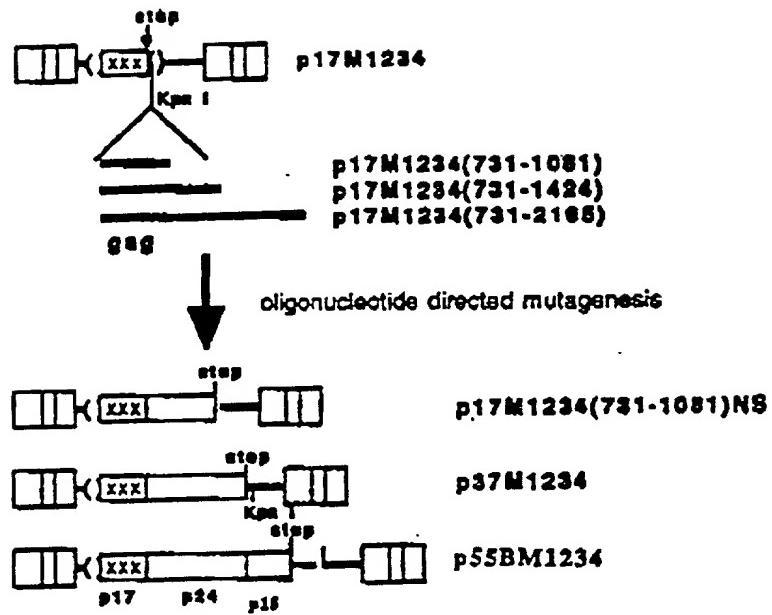


Fig. 1

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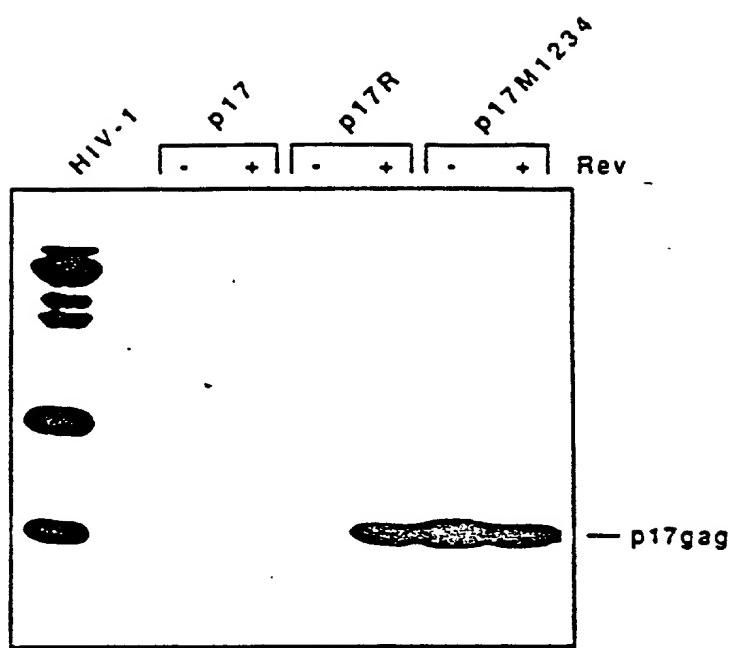
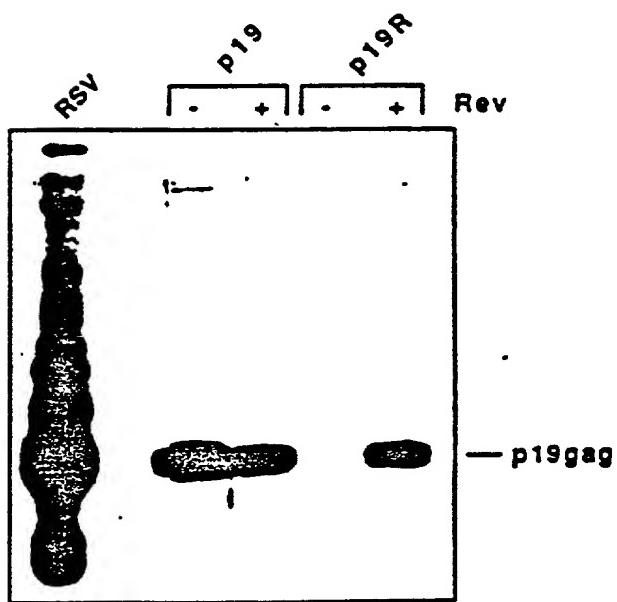
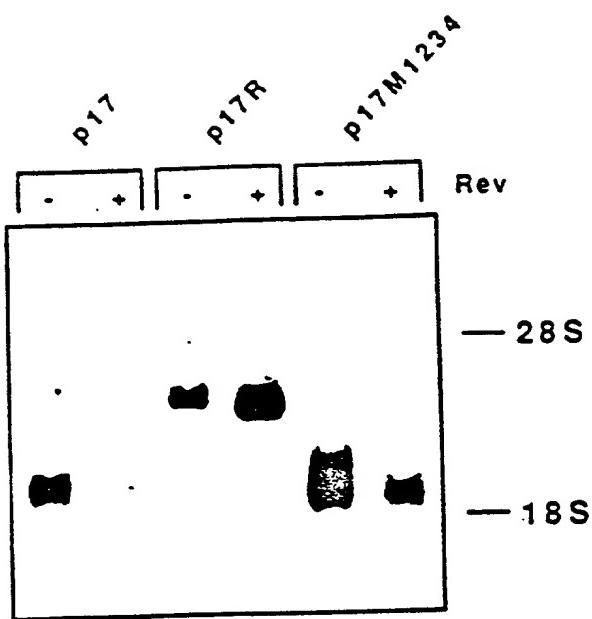
A**B**

Fig. 2

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A



B

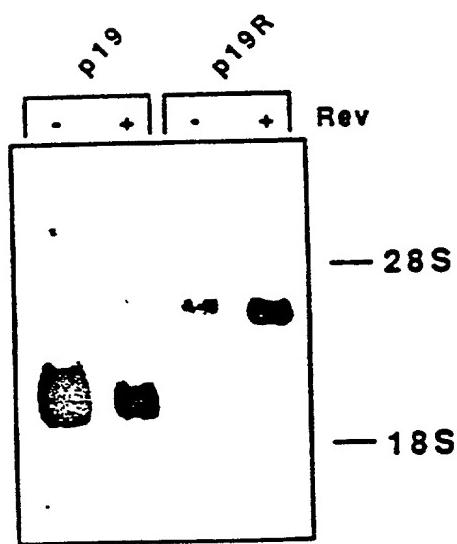


Fig. 3

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336 atg ggt gcg a_{ga} g_{cg} tca gta t_{ta} a_{gc} g_{gg} g_{ga} gaa t_{ta} gat c_{ga} t_{gg} g_{aa} a_{aa} a_{tt} c_{gg}
396 t_{ta} a_{gg} g_{ca} g_{cc} c_{gg} a_{aa} a_{aa} a_{tt} a_{aa} t_{ta} a_{aa} c_{at} a_{ta} c_{ta} t_{gg} g_{ca} a_{gc} a_{gg} g_{ag}
G G C G C G C C
456 c_{ta} g_{aa} c_{ga} t_{tc} g_{ca} g_{tt} a_{at} c_{ct} g_{gc} c_{tg} t_{ta} g_{aa} a_{ca} t_{ca} g_{aa} g_{gc} t_{gt} a_{ga} c_{aa} a_{ta}
516 c_{tg} g_{ya} c_{ag} c_{ta} c_{aa} c_{ca} t_{cc} c_{tt} c_{ag} a_{ca} g_{ga} t_{ca} g_{aa} c_{tt} a_{ga} t_{ca} t_{ta} t_{at} a_{at}
G G C C C C
576 a_{ca} c_{ta} g_{ca} a_{cc} c_{tc} t_{at} t_{tt} c_{tg} c_{at} c_{aa} a_{gg} a_{ta} g_{ac} a_{cc} a_{ag} g_{aa} g_{ct}
C G C C G
636 t_{ta} g_{ac} a_{ag} a_{ta} g_{ag} g_{aa} g_{ag} c_{aa} a_{ac} a_{aa} a_{gt} a_{ag} a_{aa} a_{aa} g_{ca} c_{ag} c_{aa} g_{ca} g_{ca} g_{ct}
G TCC G G C G
696 g_{ac} a_{ca} g_{ca} c_{ac} a_{gc} a_{at} c_{ag} g_{tc} a_{gc} c_{aa} a_{at} t_{ac}

Fig. 4

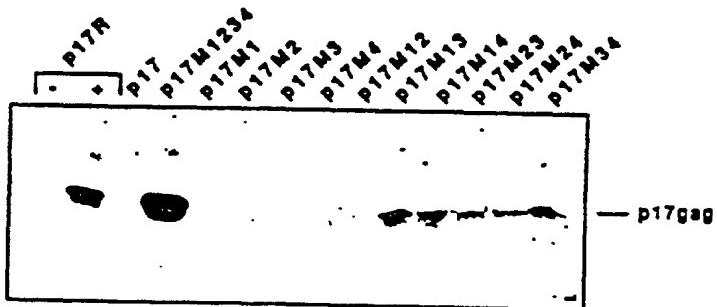
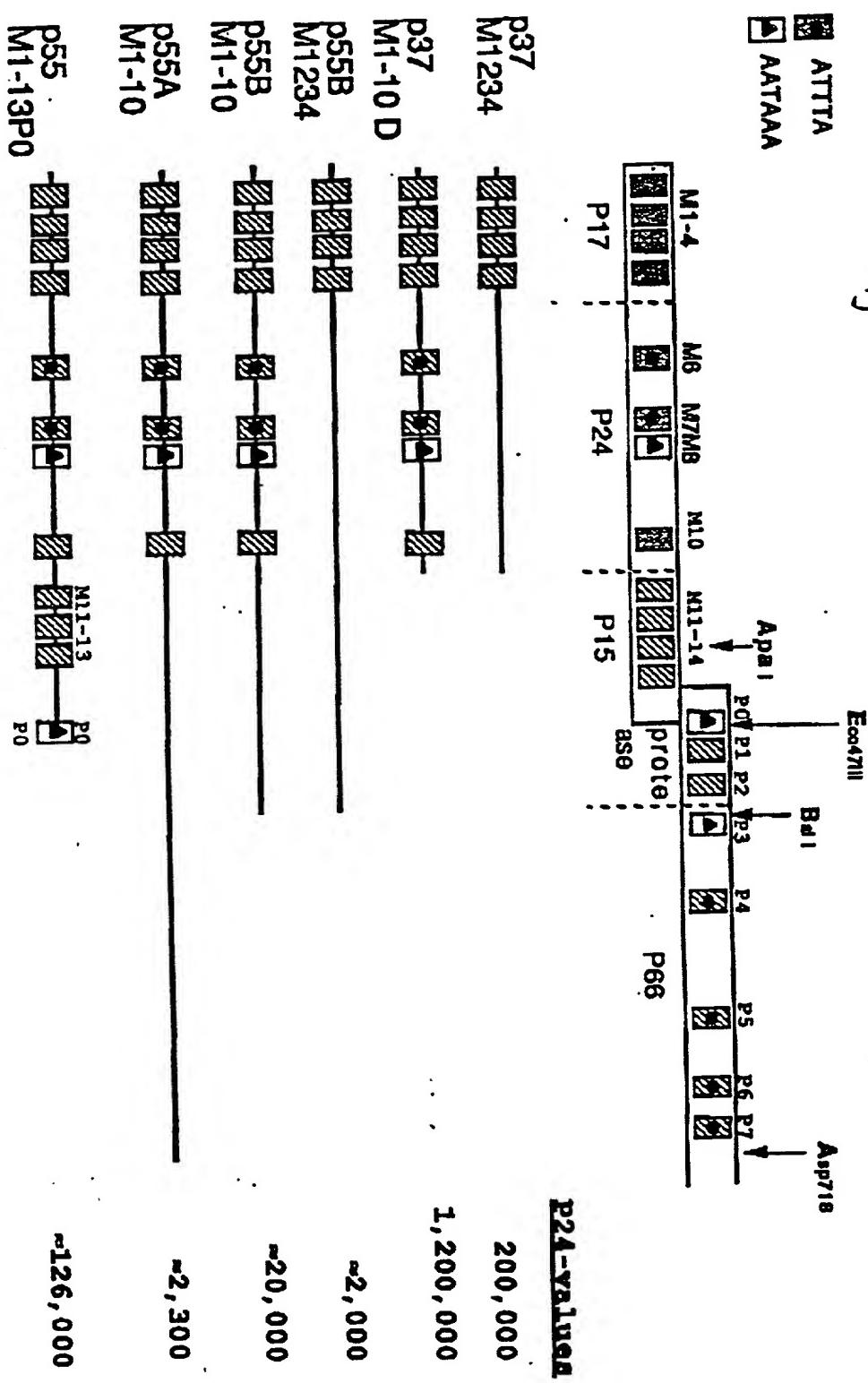


Fig. 5

Fig. 6

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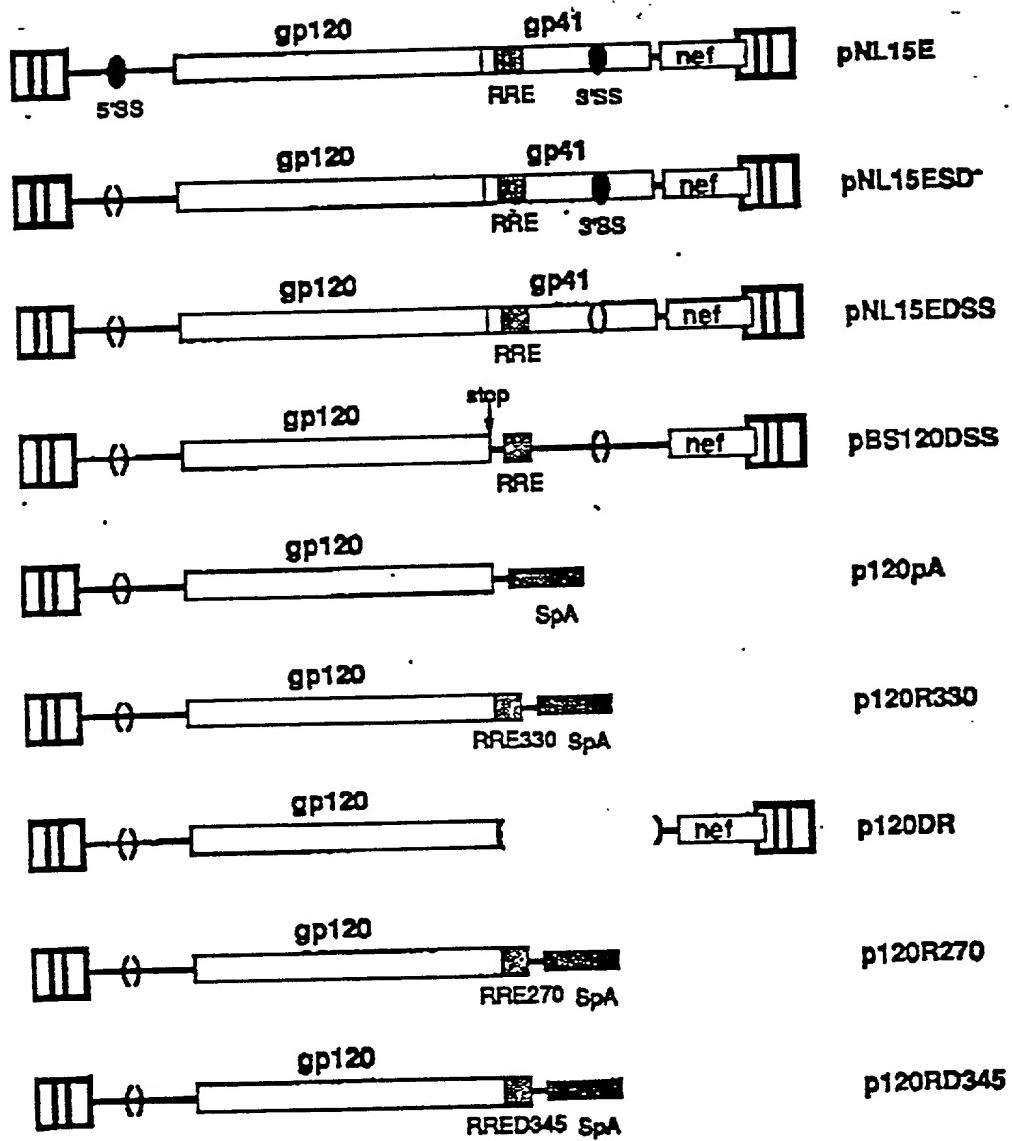


Fig. 7

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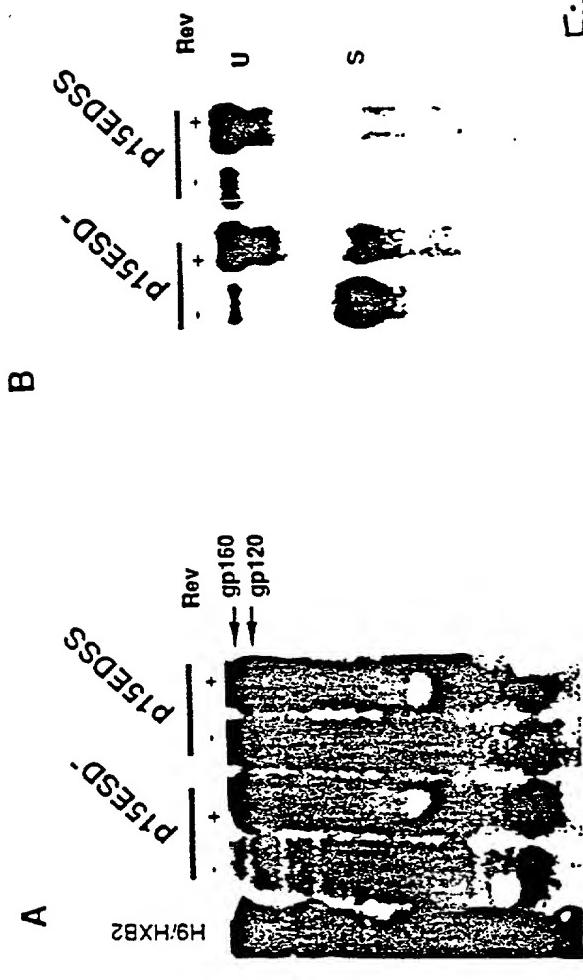
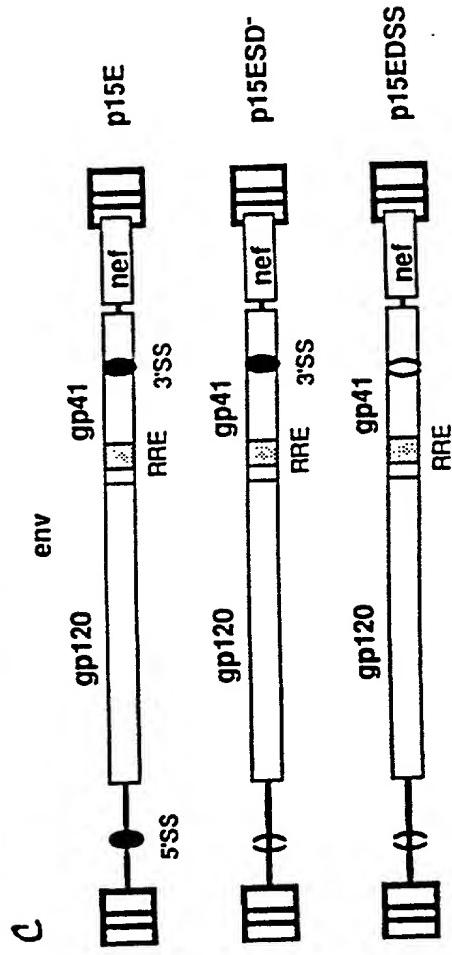
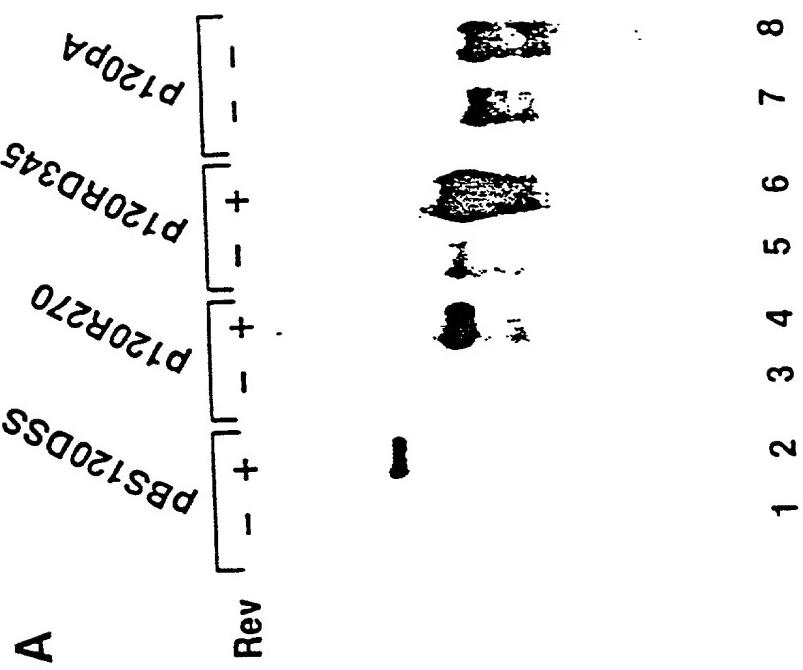


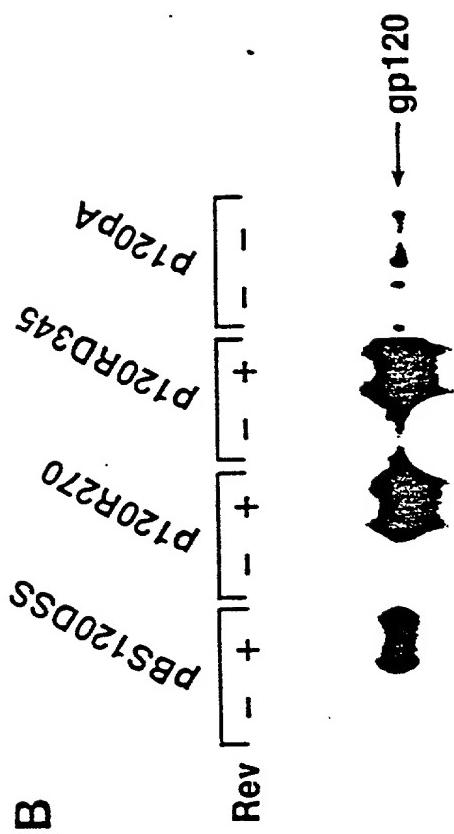
Fig. 8



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**Identification of INS regions within the
env mRNA using the p19 vector.**

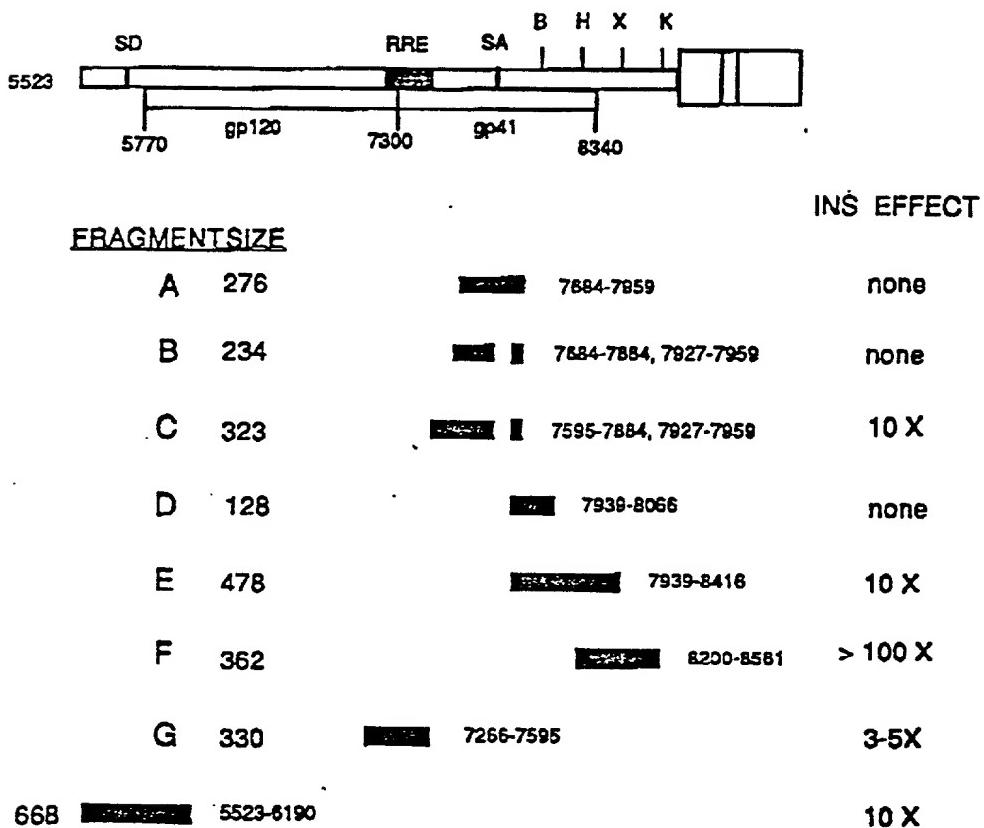


Fig. 10

**Identification of INS regions within the
env mRNA using the p37M1-10D vector.**

(fig 5 env,
formerly fig D)

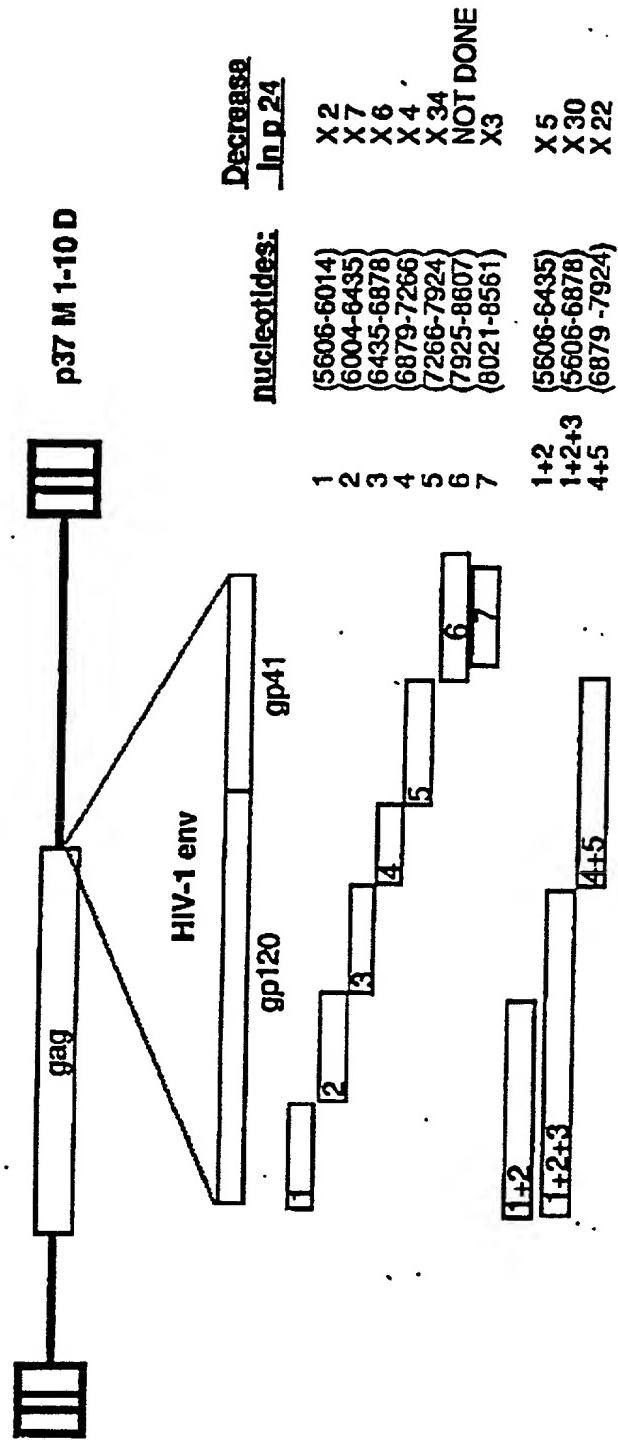
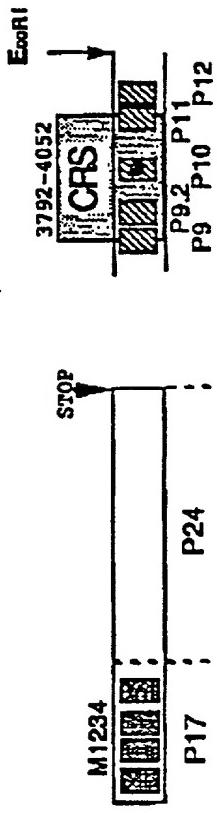


Fig. II

Elimination of negative effects of CRS

ATTIA



level of P24 expression

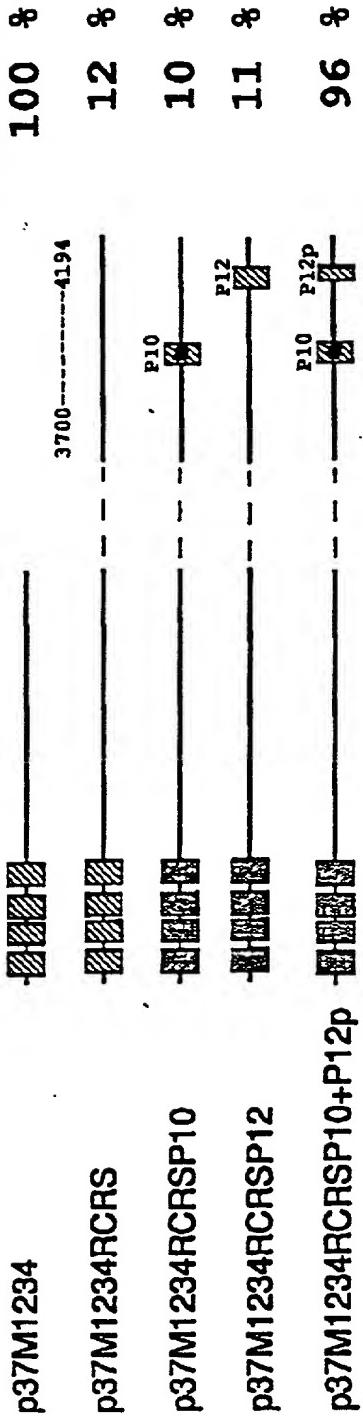


Fig. 12

POINT MUTATIONS ELIMINATING THE NEGATIVE EFFECTS OF CRS IN THE pol REGION
(nucleotides 3700-4194)

GGTACCCAGCACACAAAGGAATTGGGAAATGAAACAAGTAGATAAATTAGTCAGTGCTGGAATCAGGAAGTACTATT
TAGATGGAAATAGATAAGGCCCAAGATGAACTGAGAAATATCAGAATATCAGCTAAATTGGGAGGCAAATGGCTAGTGATTAACTCTG
CCACCTGTAGCTAGCAAAAGAAATATGAGCCAGTGTGATAAATGTCAGCTAAAGGAGAAGGCCATGGACAAAGTAA
CTGTAGTCCAGGAATATGCAACTAGATUIGTACACATTTAGAAGGAAAAGTTATCCTGGTAGCAATTCTCATGTAGCCAGTG
9 9 c 9 cc 9 9 9 9
GATATATAGAAGCAGAAGTTATCCAGCAAAACAGGGCAGGAACAGCATATTTCCTTTAAATTAAGCAGGAAAGATGG
CCAGTAAACACATACTGACAATGGCAGCAATTACCGGTGCTACGGTTAGGGCGCCTGTGGTGGCGGGAT
c 9 c a c t
CAAGCAGGAATTTCG

Fig. 13

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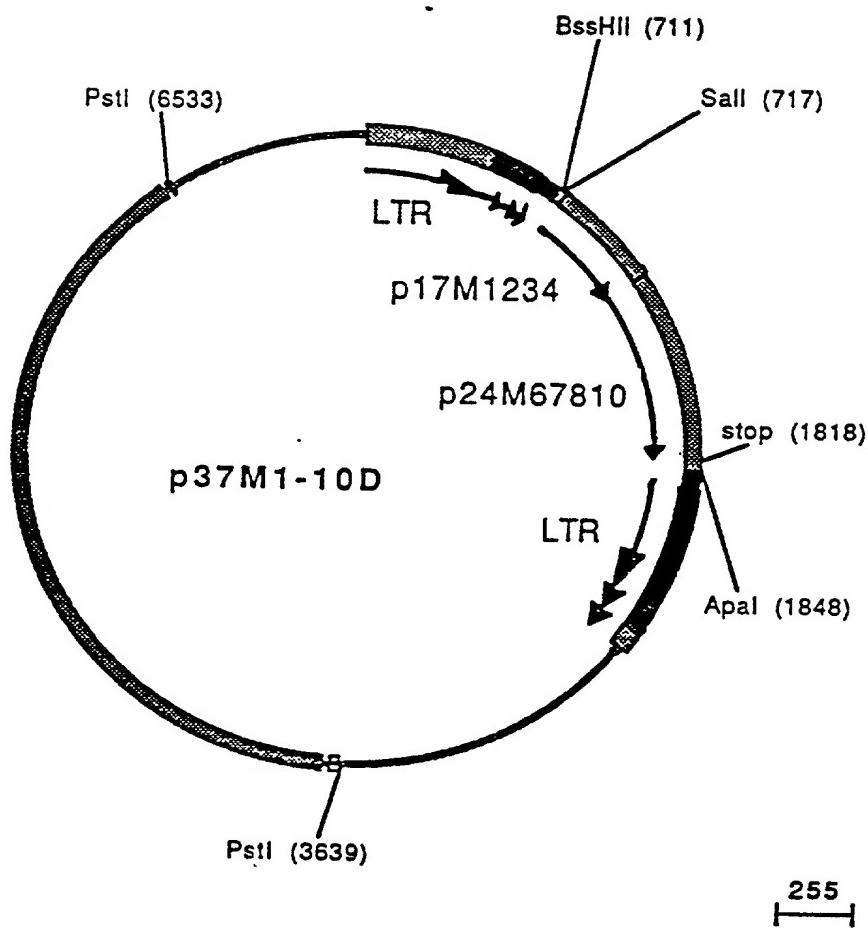


Fig. 14

A

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1 TGGAAAGGGCT AATTGGTCC CAAAAAGAC AAGAGATCCT TGATCTGTGG ATCTACCACA CACAAGGCTA
71 CTTCCCTGAT TGGCAGAACT ACACACCAGG GCCAGGGATC AGATATCCAC TGACCTTTGG ATGGTGCTTC
141 AAGTTAGTAC CAGTTGAACC AGAGCAAGTA GAAGAGGCCA AATAAGGAGA GAAGAACAGC TTGTTACACC
211 CTATGAGCCA GCATGGGATG GAGGACCCGG AGGGAGAAGT ATTAGTGTGG AAGTTTGACA GCCTCCTAGC
281 ATTTCGTCAC ATGGCCCGAG AGCTGGATCC GGAGTACTAC AAAGACTGCT GACATCGAGC TTTCTACAAG
351 GGACTTTCCG CTGGGGACTT TCCAGGGAGG TGTGGCTGG GCGGGACTGG GGAGTGGCGA GCCTCAGAT
421 GCTACATATA AGCAGCTGCT TTTGCCTGT ACTGGGTCTC TCTGGTTAGA CCAGATCTGA GCCTGGGAGC
491 TCTCTGGCTA ACTAGGGAAC CCACTGCTTA AGCCTCAATA AAGCTTGCT TGAGTGGCTCA AAGTAGTGTG
561 TGCCCCGCTG TTGTGTGACT CTGGTAACTA GAGATCCCTC AGACCCCTT AGTCAGTGTG GAAAATCTCT
631 AGCAGTGGCG CCCGAACAGG GACTTGAAG CGAAAGTAAA GCCAGAGGAG ATCTCTCGAC GCAGGACTCG
BssHII (711)
701 GCTTGCCTGAAGCGCGCGTCGACAGAGAGATGGGTGCGAGAGCGTCAGTATAAGCGGGGAGAATTAGATCGATGG
17> M e t G l y A l a R g A l a S e r V a l L e u S e r G l y G l u L e u A s p A r g T r p
777 GAAAAAAATTGGTAAAGGCCAGGGGGAAAGAAGAAGTACAAGCTAAAGCACATCGTATGGCAAGCAGGGAGCTAG
17> G l u L y s I l e A r g L e u A r g P r o G l y G l y L y s L y s L y s T y r L y s L e u L y s H i s I l e V a l T r p A l a S e r A r g G l u L e u G
853 AACGAATCGCAGTTAACCTGGCTGTAGAAACATCAGAAGGCTGTAGACAAATACTGGACACCTACAAACCATC
42> I u A r g P h e A l a V a l A s n P r o G l y L e u L e u G l u T h r S e r G l u G l y C y s A r g G l u I l e L e u G l y G l u L e u G l u P r o S e
929 CCTTCAGACAGGATCAGAGGAGCTTCGATCACTATACACACAGTAGCAACCCCTATTGTGTGCACCGCGGATC
67> r L e u G l u N T h r G l y S e r G l u G l u L e u A r g S e r L e u T y r A s n T h r V a l A l a T h r L e u T y r C y s V a l H i s G l u A r g I l e
1005 GAGATCAAGGACACCAAGGAAGCTTTAGACAAGATAGAGGAAGAGCAAACAAAGTCCAAGAAGAAGGCCAGCAGG
93> G l u I l e L y s A s p T h r L y s G l u A l a L e u A s p L y s I l e G l u G l u G l u G l u A s n L y s S e r L y s L y s A l a G l u G l u N A
1081 CAGCAGCTGACACAGGACACAGCAATCAGGTAGCCAAAATTACCCCTATAGTGCAGAACATCCAGGGCAAATGGT
118> I a A l a A l a A s p T h r G l y H i s S e r A s n G l u V a l S e r G l u A s n T D P r o l i l e V a l G l u A s n I l e G l u G l u M e t V a
1157 ACATCAGGCCATATCACCTAGAACCTTAAATGCATGGTAAAGTAGTAGAAGAGAAGGCTTCAGCCCAGAAGTG
11> I His G l u A l a I l e S e r P r o A r g T h r L e u A s n A l a T r p V a l L y s V a l V a l G l u G l u G l u L y s A l a P h e S e r P r o G l u V a l
1233 ATACCCATGTTTCAGCATTATCAGAAGGAGCCACCCACAGGACCTGAAACACGATGTGAACACCGTGGGGGAC
37> I l e P r o M e t P h e S e r A l a L e u S e r G l u G l y A l a T h r P r o G l u A s p L e u A s n T h r M e t L e u A s n T h r V a l G l y G l y H
1309 ATCAAGCAGCCATGCAAATGTTAAAGAGACCATCAATGAGGAAGCTGCAGAATGGGATAGAGTGCATCCAGTGCA
62> I s G l u A l a A l a M e t G l u M e t L e u L y s G l u T h r I l e A s n G l u G l u A l a A l a G l u U T r p A s p A r g V a l H i s P r o V a l H i
1385 TGCAGGGCTATTGCACCAGGCCAGATGAGAGAACCAAGGGAAAGTGACATAGCAGGAACACTAGTACCCCTCAG
87> s A l a G l y P r o l i l e A l a P r o G l y G l u M e t A r g G l u P r o A r g G l y S e r A s p I l e A l a G l y T h r T h r S e r T h r L e u G l u n
1461 GAACAAATAGGATGGATGACAATAATCCACCTATCCAGTAGGAGAGATCTACAAGAGGTGGATAATCCTGGGAT
113> G l u G l u I l e G l y T r p M e t T h r A s n A s n P r o P r o l i l e P r o V a l G l y G l u I l e T y r L y s A r g T r p I l e I l e L e u G l y L
1537 TGAACAAAGATCGTGGGGATGTATAGCCCTACCAGCATTCTGGACATAAGAACAGGACCAAAGGAACCCCTTAGAGA
138> G l u A s n L y s I l e V a l A r g M e t T y r S e r P r o T h r S e r I l e L e u A s p I l e A r g G l u G l u P r o L y s G l u P r o P h e A r g A s

Fig. 14 B

1613 CTATGTAGACCGGTTCTATAAAACTCTAAGAGCTGAGCAAGCTTCACAGGAGGTAAAAATTGGATGACAGAAC
 1631 pTyrValAspArgPheTyrLysThrLeuArgAlaGl uGl nAl aSer Gl nGl uVal LysAsnTrpMet Thr Gl uThr
 1689 TTGTTGGTCCAAAATGCGAACCCAGATTGTAAGACCACCTGAAGGCTCTCGGCCAGCGGCTACACTAGAAGAAA
 1891 LeuLeuVal Gl nAsnAl aAsnProAspCysLysThr IleLeuLysAlaLeuGl yProAl aAl aThr LeuGl uGl uM

STOP (1818) XbaI (1862)

1765 TGATGACAGCATGTCAGGGAGTAGGAGGACCCGGCCATAAGGCAAGACTTTGTAGGGATCCACTAGTTCTAGACT
 2141 eMet I Thr Al aCys Gl nGl yVal Gl yGl yProGl yHisLysAlaArgValLeu

Apal (1848)

1841 CGAGGGGGGG CCCGGTACCT TTAAGACCAA TGACTTACAA GGCAGCTGTA GATCTTAGCC ACTTTTTAAA
 1911 AGAAAAGGGG GGACTGGAAG GGCTAATTCA CTCCCAAAGA AGACAAGATA TCCTTGATCT GTGGATCTAC
 1981 CACACACAAG GCTACTTCCC TGATTGGCAG AACTACACAC CAGGGCCAGG GGTAGAAGAG GCCAATAAG GAGAGAACAC
 2051 TTGGATGGTG CTACAAGCTA GTACCAAGTTG AGCCAGATAA GGTAGAAGAG GCCAATAAG GAGAGAACAC
 2121 CAGCTGTAA CACCCGTGTA GCCTGCATGG AATGGATGAC CCTGAGAGAG AAGTGTAGA GTGGAGGTTT
 2191 GACAGCCGCC TAGCATTCA TCACGTGGCC CGAGAGCTGC ATCCGGAGTA CTTCAAGAAC TGCTGACATC
 2261 GAGCTTGCTA CAAGGGACTT TCCGCTGGGG ACTTTCCAGG GAGGGGTGGC CTGGGCGGGG CTGGGGAGTG
 2331 GCGAGCCCTC AGATGCTGCA TATAAGCAGC TGCTTTTGC CTGTAAGTGGG TCTCTCTGGT TAGACCAGAT

→

2401 CTGAGCCTGG GAGCTCTCTG CCTAACTAGG GAACCCACTG CTTAACGCTC AATAAAAGCTT GCCTTGAGTG
 2471 CTTCAAGTAG TGTGTCCCCG TCTGTGTGT GACTCTGGTA ACTAGAGATC CCTCAGACCC TTTTAGTCAG

→

2541 TGTGGAAAAT CTCTAGCACC CCCCAGGAGG TAGAGGTGC AGTGAACCAA GATCGCGCCA CTGCATTCCA

2611 GCCTGGCAA GAAAACAAGA CTGTCTAAAA TAATAATAAT AAGTTAAGGG TATTAATAT ATTATACAT
 2681 GGAGGTCTATA AAAATATATA TATTTGGGCT GGGCGCAGTG GCTCACACCT GCGCCCGGCC CTTTGGGAGG
 2751 CCGAGGCAAG TGGATCACCT GAGTTTGGGA GTTCCAGACC AGCCTGACCA ACATGGAGAA ACCCCCTCTC
 2821 TGTGTATTT TAGTAGATT TATTTTATGT GTATTTTATT CACAGGTATT TCTGGAAAAC TGAAACTGTT
 2891 TTCCCTCTAC TCTGATACCA CAAGAATCAT CAGCACAGAG GAAGACTTCT GTGATCAAAT GTGGTGGGAG
 2961 AGGGAGGTTT TCAACCGAC ATGAGCAGTC AGTTCTGGG CAGACTCGGC GGGTGTCCCT CGGTTCAAGT
 3031 CCAACACCGC CTGCTGGAG AGAGGTCTAGA CCACAGGGTG AGGGCTCAGT CCCCCAAGACA TAAACACCCA
 3101 AGACATAAAC ACCAACACAGG TCCACCCCCC CTGCTGCCA GGCAGAGCCG ATTCAACCAAG ACGGGAAATTA
 3171 GGATAGAGAA AGAGTAAGTC ACACAGAGCC GGCTGTGGG GAGAACCGGAG TTCTATTATG ACTCAAATCA
 3241 GTCTCCCCAA GCATCGGGG ATCAGAGTTT TTAAGGATAA CTTAGTGTGT AGGGGGCCAG TGAGTTGGAG
 3311 ATGAAAAGCT AGGGAGTCGA AGGTGTCTT TTGCGCCAG TCAGTTCTG GGTGGGGGCC ACAAGATCGG
 3381 ATGAGCCAGT TTATCAATCC GGGGGTGCCA GCTGATCCAT GGAGTGCAGG GTCTGCAAA TATCTCAAGC
 3451 ACTGATTGAT CTTAGGTTT ACAATAGTGA TGTTACCCA GGAACAATTT GGGGAAGTC AGAATCTGT
 3521 AGCCTGTAGC TGCATGACTC TAAACCATA ATTCTTTT TGTGTTTTTT TTTTATTT TGAGACAGGG

→

3591 TCTCACTCTG TCACCTAGGC TGGAGTGCAG TGGTGCATC ACAGCTCACT GCGCCCGCTA GAGCGCCGC
 3661 CACCGCCGTG GAGCTCCAAAT TCGCCCTATA GTGAGTGTAA TTACAAATTCA CTGGCCGTGCG TTTTACAACG
 3731 TCGTGACTGG GAAAACCCGTG CGTGTACCCA ACTTAATCGC CTTGCGACAC ATCCCCCTTT CGCCAGCTGG
 3801 CGTAATAGCG AAGAGGCCCG CACCGATCGC CCTTCCCCAAC AGTTGCGCAG CCTGAATGGC GAATGGCGCG
 3871 AAATTGTAAG CGTTAAATATT TTGTTAAAAT TCGCTTAAAT TTTTGTAA ATCAGCTCAT TTTTTAACCA
 3941 ATAGGCCGAAT ATCGGCAAA TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG TGTTGTTCCA
 4011 GTTTGGAAACA AGAGTCCACT ATTAAGAAGC GTGGACTCCA ACCTCAAAAGG GCGAAAAAAAC GTCTATCAGG
 4081 GCGATGGGCC ACTACGTGAA CCTACACCCCT ATCAAGTTT TTTGGGTGAG GTGCCCCGTA AAGCACTAAA
 4151 TCGGAACCCCT AAAGGGAGCC CCCGATTTAG AGCTGACGG GGAAAGCCCG CGAACGTGGC GAGAAAGGAA
 4221 GGGAAAGAAAG CGAAAGGAGC GGGCGCTAGG GCGCTGGCAA GTGTAGGGT CACGCTGCGC GTAACACCA
 4291 CACCCGCCGC GCTTAATGCG CCGCTACAGG GCGCGTCCCA GGTGGCACTT TTGGGGAAA TGTCGCCGG
 4361 ACCCTATTT GTTTATTTT TAAATATGT ATCCGCTCAT GAGACAATAA CCTGATAAA

→

PstI (3639)

Fig. 14 C

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4431 TGCTTCAATA ATATTGAAAA AGGAAGACTA TGAGTATTCA ACATTCGGT GTGCCCTTA TTCCCTTTT
4501 TCGGGCATTT TGCCTTCCTG TTTTGCTCA CCCAGAAACG CTGGTAAAG TAAAGATGC TGAAGATCAG
4571 TTGGGTGCAC GAGTGGGTTA CATCGAAGT GATCTCAACA GCGGTAAGAT CCTTGAGAGT TTGCCCCCG
4641 AAGAACGTTT TCCAATGATG AGCACTTTA AAGTTCCTGCT ATGTGGGGG GTATTATCCC GTATTGACGC
4711 CGGGCAAGAG CAACTCGGTC GCCGCATACA CTATTCTAG AATGACTTGG TTGAGTACTC ACCAGTCACA
4781 GAAAAGCATC TTACGGATGG CATGACAGTA AGAGAATTAT GCAGTGCCTGC CATAACCATG AGTGATAACA
4851 CTGCGGCCAA CCTACTTCTG ACAACGATCG GAGGACCGAA GGAGCTAACCC GCTTTTTGC ACAACATGGG
4921 GGATCATGTA ACTCGCCCTG ATCGTTGGGA ACCGGAGCTG AATGAAGCCA TACCAAACGA CGAGCGTGAC
4991 ACCACGATGC CTGTACCAAT GGCAACAAACG TTGCGCAAAC TATTAACCTGG CGAACTACTT ACTCTAGCTT
5061 CCCGGCAACA ATTAATAGAC TTGGATGGGG CGGATAAAGT TGCAAGGACCA CCTCTGCCTCG CCGCCCTTC
5131 GGCTGGCTGG TTATGCTG ATAAATCTGG AGCGGTGAG CGTGGGTCTC CGGGTATCAT TGCAAGCACTG
5201 GGGCAGATG GTAAGCCTC CGGTATCGTA GTTATCTACA CGACGGGGAG TCAGGCAACT ATGGATGAAAC
5271 GAAATAGACA GATCGCTGAG ATAGGTGCCT CACTGATTA GCATGGTAA CTGTCAGACC AGTTTACTC
5341 ATATATACCT TAGATTGATT TAAAACCTCA TTTTTAATT AAAAGGATCT AGGTGAAGAT CCTTTTGTAT
5411 AATCTCATGA CCAAATCCC TTAACGTGAG TTTTCGTTCC ACTGAGCGTC AGACCCCGTA GAAAAGATCA
5481 AAGGATCTTC TTGAGATCCT TTTTTCTGC CGGTAACTCG CTGCTTGCAA ACAAAAAAAC CACCGCTTAC
5551 AGCGGTGGTT TGTTCGCCGG ATCAAGAGCT ACCAACCTTT TTTCCGAAAGG TAACTGGCTT CAGCAGAGCG
5621 CAGATACCAA ATATGTCCT TCTAGTGTAG CGGTAGTTAG GCCACCAACTT CAAGAACTCT GTAGCACCCG
5691 CTACATACCT CGCTCTGCTA ATCCCTGTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
5761 GTGGACTCA AGACCATGATG TACCGGATAA GGCGCAGCGG CGGGGCTGAA CGGGGGGTTG GTGCACACAG
5831 CCCAGCTTGG AGCGAACGAC CTACACCGAA CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC
5901 TCCCCGAGG GAGAAAGGGCG GACAGGTATC CGGTAAAGCGG CAGGGCTCGA ACAGGAGAGC GCACGAGGG
5971 GCTTCCAGGG GGAAACGCCCT GGTATCTTA TAGTCTGTC GGGTTTCGCC ACCTCTGACT TGAGCGTCGA
6041 TTTTTGTGAT GCTCGTCAGG GGGGGCGAGC CTATGGAAA ACGCCAGCAA CGCGGCCCTT TTACGGTTCC
6111 TGGCCTTTTG CTGGCTTTT GCTCACATGT TCTTCTGC TTATCCCTT GATTCTGTGG ATAACCGTAT
6181 TACCGCTTTG GAGTGGCTG ATACCGCTCG CGCGCAGCGA ACGACCGAGC GCAGCGAGTC AGTGAGCGAG
6251 GAAGCGGAAG AGCCCAAT ACGCAACCCG CCTCTCCCCG CGCGTTGGCC GATTCACTAA TGAGCTGGC
6321 ACGACAGGTT TCCCCACTGG AAAGCGGGCA GTGAGCGCAA CGCAATTAAAT GTGAGTTAGC TCACTCATTA
6391 GGCACCCCAAG GCTTACACT TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATT
6461 CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTCG GAATTAACCC TCACTAAAGG GAACAAAAGC

PstI (6533)

6531 TGCTGCAGGG TCCCTTAACCTG CCAAGCCCCA CAGTGTGCC TGAGGCTGCC CCTTCCCTCT AGCGGCTGCC
6601 CCCACTCGGC TTGCTTTCC CTAGTTTCAG TTACTTGCGT TCAGCCAAGG TCTGAAACTA GGTGCGCACA
6671 GAGCGGTAAAG ACTGGAGAG AAAGAGACCA GCTTACAGG GGGTTATCA CAGTGCACCC TGACAGTCGT
6741 CAGCCTACAA GGGGGTTTAT CACATTGAC CCTGACAGTC GTCAAGCTCA CAGGGGGTTT ATCACAGTGC
6811 ACCCTTACAA TCATTCCATT TGATTACAA TTTTTTAGT CTCTACTGTG CCTAACTTGT AGTTAAATT
6881 TGATCAGAGG TGTGTTCCCA GAGGGGAAAA CAGTATATAC AGGGTTAGT ACTATCGCAT TTCAAGGCC
6951 CACCTGGTCA TTGAATGTG TCCCCCGAGG GGTGATGACT ACCTCAGTTG GATCTCCACA GGTACAGTG
7021 ACACAAGATA ACCAAGACAC CTCCCAAGGC TACCCACAATG GGCGCCCTC CACGTGCACA TGGCCGGAGG
7091 AACTGCCATG TCGGAGGTGC AAGCACACCT GCGCATCAGA GTCCCTGGTG TGGAGGGAGG GACCAGCGCA
7161 GCTTCCAGGC ATCCACCTGA TGACAGAAC CTAGGGAAAG CCCCAGTCT ACTTACACCA GGAAAGGC

Fig. 14 D